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(54) DNA FRAGMENT, RECOMBINATION VECTOR CONTAINING THE SAME, AND METHOD OF THE EXPRESSION OF ALIEN GENE WITH THE USE OF THE SAME

(57) A novel DNA which has a sequence different from those of publicly known DNAs capable of promoting the expression of an alien gene and can remarkably promote the expression of an alien gene. An isolated DNA fragment having a base sequence represented by SEQ ID NO:1 in the Sequence Listing; and an isolated

DNA fragment represented by this base sequence wherein one or more nucleotides have been added, inserted, deleted or replaced and having the effect of promoting the expression of a gene located in the downstream thereof.

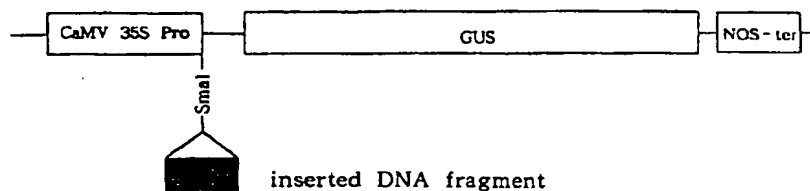


Fig. 1

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Description**TECHNICAL FIELD**

5 The present invention relates to a novel DNA fragment having function to promote expression of genes, a vector containing the same and a method for expressing foreign genes using the same.

BACKGROUND ART

10 Promotion of expression of foreign genes is one of the most important techniques in applying genetic engineering processes to plants. One of the methods therefor is utilization of a DNA having a nucleotide sequence which promotes expression of a gene.

Known nucleotide sequences which promote expression of foreign genes include the intron of the catalase gene of castor bean (Japanese Laid-open Patent Application (Kokai) No. 3-103182; Tanaka et al., Nucleic Acids Res. 18, 6767-6770 (1990)). However, since there are wide varieties of plants to be manipulated and since promotion of expression of genes is required in each of the desired growth stages or tissues of organs, it is desired that wide varieties of DNAs which promote expression of genes can be utilized.

DISCLOSURE OF THE INVENTION

20 Accordingly, an object of the present invention is to provide a novel DNA, which can promote expression of foreign genes and which has a nucleotide sequence different from those of known DNAs that promote expression of foreign genes.

The present inventors intensively studied to discover introns of rice phospholipase D (hereinafter also referred to as "PLD") gene by comparing a rice cDNA and a rice genomic DNA, and discovered that one of the introns has a function to prominently promote expression of the gene downstream thereof, thereby completing the present invention.

25 That is, the present invention provides an isolated DNA fragment having a nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing or having a nucleotide sequence which is the same as the nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing except that one or a plurality of nucleotides are added, inserted, deleted or substituted, the latter nucleotide sequence having a function to promote expression of a gene downstream thereof. The present invention also provides a recombinant vector comprising the above-mentioned DNA fragment according to the present invention and a foreign gene to be expressed, which is operably linked to the DNA fragment at a downstream region of the DNA fragment. The present invention further provides a method for expressing a foreign gene comprising introducing the recombinant vector according to the present invention into host cells and expressing the foreign gene.

30 As experimentally confirmed in the Example described below, the DNA fragment according to the present invention largely promotes expression of the gene downstream of the DNA fragment. Therefore, it is expected that the present invention will largely contribute to expression of foreign genes by genetic engineering processes.

BRIEF DESCRIPTION OF THE DRAWINGS

40 Fig. 1 shows the important part of a genetic map of pBI221 into which the DNA fragment according to the present invention is inserted, which was prepared in the Example of the present invention.

BEST MODE FOR CARRYING OUT THE INVENTION

45 As mentioned above, the DNA fragment according to the present invention has a nucleotide sequence shown in SEQ ID NO. 1 in the Sequence Listing. As will be described in detail in the Example below, introns located upstream of rice PLD gene were identified by comparing the nucleotide sequence of the cDNA of rice PLD gene and that of the rice genomic DNA. A fragment containing one of these intron sequences having a size of 173 bp located at the 5'-flanking region was prepared by PCR and the DNA fragment was inserted into an upstream site of a reporter gene of an expression vector containing the reporter gene. By checking the expression activity of the reporter gene, it was confirmed that the DNA fragment has a function to promote expression of the gene downstream thereof. The nucleotide sequence of the DNA fragment according to the present invention corresponds to 1661nt to 1843nt of the nucleotide sequence of the rice genomic PLD gene, which nucleotide sequence is shown in SEQ ID NO. 3 of the Sequence Listing.

50 The nucleotide sequence of the above-mentioned intron sequence having a size of 173 bp, which is located upstream of the rice PLD gene, is shown in SEQ ID NO. 4 in the Sequence Listing. Needless to say, the sequence shown in SEQ ID NO. 4 also has a function to promote expression of the gene downstream thereof. The nucleotide sequence shown in SEQ ID NO. 4 corresponds to 1666nt to 1838nt of the nucleotide sequence of the rice genomic PLD gene, which is shown in SEQ ID NO. 3 in the Sequence Listing.

Since the DNA fragment according to the present invention is an intron existing upstream of the rice PLD gene, and since its nucleotide sequence was determined according to the present invention, the DNA fragment may easily be prepared by PCR using the rice genomic DNA as a template. PCR is a conventional technique widely used in the field of genetic engineering and a kit therefor is commercially available, so that those skilled in the art can easily perform the PCR. One concrete example thereof is described in detail in the Example below.

It is well-known in the art that there are cases wherein the physiological activity of a physiologically active DNA sequence is retained even if the nucleotide sequence of the DNA is modified to a small extent, that is, even if one or more nucleotides are added, inserted, deleted or substituted. Therefore, DNA fragments having the same nucleotide sequence as shown in SEQ ID NO. 1 except that the DNA fragments have such modifications, which have the function to promote expression of the gene downstream thereof, are included within the scope of the present invention. That is, the DNA fragments having the same nucleotide sequence as shown in SEQ ID NO. 1 except that one or more nucleotides are added, deleted or substituted, which have the function to promote expression of the gene downstream thereof, are included within the scope of the present invention. Particularly, in the nucleotide sequence shown in SEQ ID NO. 1, the 5 nucleotides at the 5'-end and the 6 nucleotides at the 3'-end are the nucleotides in the exon regions, so that it is thought that the nucleotide sequences which do not have these regions also have the function to promote gene expression. Thus, these DNA fragments are within the scope of the present invention.

Modification of DNA which brings about addition, deletion or substitution of the amino acid sequence encoded thereby can be attained by the site-specific mutagenesis which is well-known in the art (e.g., Nucleic Acid Research, Vol. 10, No. 20, p6487-6500, 1982). In the present specification, "one or a plurality of nucleotides" means the number of nucleotides which can be added, deleted or substituted by the site-specific mutagenesis.

Site-specific mutagenesis may be carried out by, for example, using a synthetic oligonucleotide primer complementary to a single-stranded phage DNA except that the desired mutation as follows. That is, using the above-mentioned synthetic oligonucleotide as a primer, a complementary chain is produced by a phage, and host bacterial cells are transformed with the obtained double-stranded DNA. The culture of the transformed bacterial cells is plated on agar and plaques are formed from a single cell containing the phage. Theoretically, 50% of the new colonies contain the phage having a single-stranded chain carrying the mutation and remaining 50% of the colonies contain the phage having the original sequence. The obtained plaques are then subjected to hybridization with a kinase-treated synthetic probe at a temperature at which the probe is hybridized with the DNA having exactly the same sequence as the DNA having the desired mutation but not with the original DNA sequence that is not completely complementary with the probe. Then the plaques in which the hybridization was observed are picked up, cultured and the DNA is collected.

In addition to the above-mentioned site-specific mutagenesis, the methods for substituting, deleting or adding one or more amino acids without losing the function include a method in which the gene is treated with a mutagen and a method in which the gene is selectively cleaved, a selected nucleotide is removed, added or substituted and then the gene is ligated.

The DNA fragment according to the present invention has a function to promote expression of the gene downstream thereof. Therefore, by inserting the DNA fragment according to the present invention into the transcriptional region of a desired foreign gene to be expressed, preferably into the 5'-end region of the transcriptional region, expression of the foreign gene is promoted. The method for expressing a foreign gene has already been established in the field of genetic engineering. That is, by inserting the desired foreign gene into a cloning site of an expression vector, introducing the resulting vector into host cells and expressing it, the foreign gene may be expressed. According to the method of the present invention, the DNA fragment according to the present invention is inserted at a site upstream of the foreign gene in a manner such that the DNA fragment is operably linked to the foreign gene, and the foreign gene is expressed. The term that the DNA fragment according to the present invention is "operably linked" to the foreign gene means that expression of the foreign gene is detectably increased by inserting the DNA fragment according to the present invention when compared with the case wherein the DNA fragment according to the present invention is not inserted. The DNA according to the present invention may be inserted into the site immediately upstream of the foreign gene. Alternatively, another sequence may be located between the DNA according to the present invention and the foreign gene. Although the size of this intervening sequence is not restricted, it usually has a size of 0 - 1000 bp. A promoter sequence is located upstream of the DNA fragment according to the present invention. The DNA fragment according to the present invention may be inserted into the site immediately downstream of the promoter, or another sequence may be located between the promoter and the DNA according to the present invention. Although the size of this intervening sequence is not restricted, it is usually 0 - 1000 bp. In summary, all recombinant vectors with which the expression of the foreign gene is detectably increased by inserting the DNA fragment according to the present invention when compared with the case wherein the DNA fragment is not inserted, are within the scope of the present invention.

Since the nucleotide sequence of the cloning site of an expression vector is known, the DNA fragment according to the present invention may easily be inserted into the vector.

Wide varieties of such an expression vector are well-known in the art and are commercially available. These expression vectors contain at least a replication origin for replication in the host cells, a promoter, a cloning site giving a restriction site for inserting the foreign gene, and a selection marker such as drug resistance, and usually contain a

terminator which stably terminates transcription, and an SD sequence when the host is a bacterium. In the method of the present invention, any of these known expression vectors may be employed.

Example

The present invention will now be described in more detail by way of examples thereof. However, the present invention is not restricted to the examples.

1. Purification of PLD of Rice Bran

For purification, a reference (Takano et al., Journal of Japan Food Industry Association, 34, 8-13 (1987) was referred. The enzyme activity was measured by employing phosphatidylcholine as a substrate and quantifying the choline generated by the enzyme reaction (Imamura et al., J. Biochem. 83, 677-680 (1978)). It should be noted, however, the enzyme reaction was stopped by heat treatment at 95°C for 5 minutes.

That is, to 100 g of bran of rice (*Oryza sativa*), variety "KOSHIHIKARI", one liter of hexane was added and the mixture was stirred for a whole day and night, thereby defatting the rice bran. To the resultant, 10 g of Polycral AT (trade-mark, polyvinylpyrrolidone, commercially available from GAF Chemical) and 500 ml of 10 mM Tris-HCl buffer (pH7) containing 1 mM CaCl_2 and 5 mM 2-mercaptoethanol were added, and the resulting mixture was stirred for 1 hour to extract the enzyme. The extract was filtered through an 8-layered gauze and the filtrate was centrifuged at 15,000 x g for 20 minutes, followed by recovering the middle layer as a crude extract. The crude extract was treated with ammonium sulfate (65% saturation) and the generated precipitates were collected by centrifugation (15,000 x g, 20 minutes), followed by dialyzing the precipitates after dissolution against the above-mentioned buffer. After the dialysis, precipitates were eliminated by filtration to obtain ammonium sulfate fraction.

The ammonium sulfate fraction was applied to a column (2.0 x 10 cm) of DEAE-Cellulose (commercially available from Whatman) equilibrated with buffer A (10 mM Tris-HCl, pH 7, 1 mM CaCl_2 , 1 mM 2-mercaptoethanol). After washing the column with about 100 ml of buffer A containing 50 mM NaCl, elution was carried out with 120 ml of buffer A having a linear gradient of NaCl concentration from 50 mM to 350 mM. PLD was eluted at a NaCl concentration of about 0.2 M. The fraction having PLD activity was collected as an eluted solution (DEAE-cellulose).

To the eluted solution (DEAE-cellulose), 3 M ammonium sulfate was added in an amount attaining the final concentration of ammonium sulfate of 1 M, and the resulting mixture was applied to a Phenyl Sepharose column (commercially available from Pharmacia, 2.6 x 10 cm) equilibrated with buffer A containing 1 M ammonium sulfate. Elution was performed using 240 ml of buffer A having a linear gradient of ammonium sulfate concentration from 1.0 M to 0 M. PLD was eluted at a concentration of ammonium sulfate of about 0.1 M. The fraction having the activity was recovered and dialyzed against buffer A to obtain an eluted solution (Phenyl Sepharose).

The eluted solution (Phenyl Sepharose) was applied to Mono Q column (anion-exchange column commercially available from Pharmacia, 16 x 10 cm) equilibrated with buffer A, and elution was performed using 150 ml of buffer A having a gradient of NaCl concentration from 50 mM to 350 mM. PLD was eluted at NaCl concentration from 210 mM to 235 mM. The fraction having PLD activity was recovered and dialyzed against buffer A to obtain an eluted solution (Mono Q 1st).

The eluted solution (Mono Q 1st) was concentrated to 0.5 ml by ultrafiltration and applied to Superose 6 column (commercially available from Pharmacia, 1.0 x 30 cm) equilibrated with buffer A containing 0.1 M NaCl and elution was performed using the same buffer. The molecular weight of PLD was estimated to be 78 kDa. The fraction having PLD activity was recovered as an eluted solution (Superose 6).

To the eluted solution (Superose 6), 2.5 ml of 40% Carrier Ampholite (commercially available from Pharmacia, pH4.0-6.0) and distilled water were added to attain a final volume of 50 ml and isoelectric electrophoresis was carried out using Rotofore (commercially available from Biorad). Electrophoresis was performed at 2°C with a constant power of 12W for 4 hours. PLD activity was observed at about pH 4.9. The fraction having PLD activity was collected and dialyzed against buffer A to obtain an isoelectric electrophoresis fraction.

The isoelectric electrophoresis fraction was applied to Mono Q column (commercially available from Pharmacia, 0.5 x 5 cm) and eluted with NaCl having a linear gradient of concentration of 50 mM to 350 mM. PLD was eluted at NaCl concentrations of about 210 mM and about 235 mM. The two fractions having PLD activity were recovered as eluted solutions (Mono Q 2nd-I, II).

Purities of the eluted solutions (Mono Q 2nd-I, II) were checked by SDS-polyacrylamide electrophoresis (Laemmli (1970)) using 7.5% acrylamide. After the electrophoresis, the gel was stained with Coomassie brilliant blue R-250. With either eluted solution, a main band was observed at a position corresponding to a molecular weight of 82 kDa. With the eluted solution (Mono Q 2nd-II), only a single band was observed.

By the purification described above, the purification magnifications of the eluted solutions (Mono Q 2nd-I, II) were 380 times and 760 times, respectively, with respect to the crude extract.

Properties of the enzymes contained in the two fractions were determined. The results are shown in Table 1. The

buffer solutions used for the measurement of the optimum pH were sodium acetate (pH 4-6), MES-NaOH (pH 5.5-7.0) and Tris-HCl (pH 7-9), all of which have a concentration of 100 mM in all of the buffer solutions. The pH stability means the pH range in which decrease in the enzyme activity is not observed after leaving the enzyme at the respective pH at 25°C for 30 minutes. The temperature stability was measured by measuring the remaining activity after leaving the enzyme to stand at 4°C, 25°C, 37°C or 50°C for 30 minutes. The substrate specificity was measured at a substrate concentration of 5 mM and expressed in terms of the relative activity taking the enzyme activity to phosphatidylcholine as 100.

Table 1

	Mono Q 2nd-I	Mono Q 2nd-II
Km Value	0.29 mM	0.29 mM
Optimum pH	6	6
pH Stability	7-8	7-8
Temperature Stability	4-37°C	4-37°C
Ca ²⁺ Dependency	not less than 20 mM	not less than 20 mM
Substrate Specificity		
Phosphatidylcholine	100	100
Lysophosphatidylcholine	13	12
Sphingomyelin	6	4

2. Proof that Purified Protein is PLD

Each of the eluted solutions (Mono Q 2nd-I, II) was subjected to SDS-polyacrylamide gel electrophoresis in the same manner as in the purity test, and the obtained patterns were transferred to PVDF membranes (commercially available from Millipore), followed by staining the membranes. The band of the protein having the molecular weight of 82 kDa was cut out and the amino acid sequence of the N-terminal region of the protein was determined by a protein sequencer (commercially available from Shimazu Seisakusho, PSQ-1). For both proteins, amino acid sequence up to 10 residues from the N-terminal could be determined, and the determined sequences were identical. The sequence was as follows. Val Gly Lys Gly Ala Thr Lys Val Tyr Ser

Although the relationship between the proteins having the molecular weight of 82 kDa contained in the two fractions having the enzyme activity is not clear, it is thought that they have high homology in their amino acid sequences, so that it was judged that there would be no problem even if a mixture of the fractions is used as an antigen for preparing an antibody.

A mixture of the eluted solutions (Mono Q 2nd-I, II) was subjected to SDS-polyacrylamide gel electrophoresis using 7.5% acrylamide, and the gel was stained with Coomassie brilliant blue R-250. The band of the protein having the molecular weight of 82 kDa was cut out and recovered by electroelution (25 mM Tris, 192 mM glycine, 0.025% SDS, 100V, 10 hours). Then SDS was removed by electroelution (15 mM ammonium bicarbonate, 200 V, 5 hours) and the resultant was lyophilized. For the electroelution and electroelution, BIOTRAP (commercially available from Schleicher & Schuell) was used.

The protein having the molecular weight of 82 kDa highly purified by the above-described method was administered to a rabbit in an amount of 50 µg per time at 7 days' intervals. Immunological titration test was performed for the sera before the immunization and after the third immunization. To the PLD solution containing 8.6×10^{-3} units of PLD, were added 0 - 50 µl of the serum before the immunization or after the third immunization, 50 µl of 250 mM Tris-HCl (pH 7.0), 5 µl of 50 mM CaCl₂, 50 µl of 0.2% Triton X-100 (trademark) and water to a total volume of 250 µl, and the mixture was left to stand at room temperature for 2.5 hours. To the resultant, 200 µl of Protein A Sepharose (commercially available from Pharmacia) was added and the resulting mixture was gently shaken at room temperature for 2 hours. The mixture was then centrifuged (500 x g, 5 minutes) and the enzyme activity in the supernatant was measured. Taking the measured enzyme activity in the case where the serum was not added as 100%, the enzyme activities in cases where 20 µl and 50 µl of the serum before immunization were added were 95% and 88%, respectively, and the enzyme activities in cases where 20 µl and 50 µl of the serum after the third immunization were added were 75% and 30%, respectively. These results prove that the protein having the molecular weight of 82 kDa is PLD.

3. Determination of Amino Acid Sequence of Internal Regions

The PLD protein was fragmented in a gel (Cleveland et al., J. Biol. Chem., 252, 1102(1977)). The cut out gel containing the PLD protein was inserted into a stacking gel well on a 15% acrylamide gel prepared for separation of peptides, and *Staphylococcus aureus* V8 protease (commercially available from Wako Pure Chemical Industries, Ltd) in an amount of 1/10 volume of the PLD protein was overlaid, followed by starting electrophoresis. The electrophoresis was stopped at the time point at which the bromophenol blue reached the center of the stacking gel and then restarted 30 minutes later. After the electrophoresis, the pattern was transferred to a PVDF membrane and the membrane was stained. Clear bands were observed at the positions corresponding to molecular weights of 20, 14, 13, 11 and 10 kDa. Each of the bands of the peptide fragments having molecular weights of 20, 14 and 13 kDa were cut out and their amino acid sequences were determined by a protein sequencer. The determined sequences are as follows.

20 kDa	Asn Tyr Phe His Gly Ser Asp Val Asn ? Val Leu ? Pro Arg Asn Pro Asp Asp(Asp) ? ? Ile
14 kDa	Thr ? Asn Val Gln Leu Phe Arg Ser Ile Asp Gly Gly Ala Ala Phe Gly Phe Pro Asp Thr Pro Glu Glu Ala Ala
13 kDa	Ile Ala Met Gly Gly Tyr Gln Phe Tyr His Leu Ala Thr Arg Gln Pro Ala Arg Gly Gln Ile His Gly Phe Arg Met Ala
	Leu ? Tyr Glu His Leu Gly Met Leu ? Asp Val Phe

(In the sequences, "?" means the amino acid residue which could not be identified, and the amino acid residue in parentheses means that the amino acid residue could not be identified confidentially.

4. Preparation of cDNA Library of Rice Immature Seeds

Total RNAs were extracted from immature seeds obtained after 5 days from flowering by the SDS-phenol method, and prepared by the lithium chloride precipitation. Poly(A)⁺RNA was prepared using Oligotex-dT30 (commercially available from Takara Shuzo) according to the instructions provided by the manufacturer. For the cDNA cloning, cDNA synthesis System Plus (commercially available from Amersham) and cDNA Cloning System λ gt10 (commercially available from Amersham) were used. However, λ ZAPII vector (commercially available from Stratagene) was used as the cloning vector and XL1-Blue was used as the host cells.

5. Preparation of Probes

Oligonucleotides corresponding to the amino acid sequences of PLD were synthesized by a DNA synthesizer (commercially available from Applied Biosystems). The sequences thereof as well as the corresponding amino acid sequences are as follows.

20KF	5' AAYTAYTTYCAYGG 3'
20KR1	5' RTCRTCRTCNGGRTT 3'

(In these sequences, "R" represents a purine base A or G; "Y" represents a pyrimidine base T or C; and N represents G, A, T or C.)

The 20KF is a mixture of 32 kinds of oligonucleotides containing the DNA sequences encoding the amino acid sequence of

Asn Tyr Phe His Gly

found in a peptide having a molecular weight of 20 kDa, and the 20KR1 is a mixture of 128 kinds of oligonucleotides containing complementary chains of the DNA sequences encoding the amino acid sequence of

Asn Pro Asp Asp(Asp)

found in the same peptide.

The cDNA synthesis was carried out using 10 ng of Poly(A)⁺RNA, 0.3 μ g of random hexamer (N6), 10 U of an RNase inhibitor (RNA Guard, commercially available from Pharmacia), 1 mM each of dATP, dCTP, dGTP and dTTP, 1 x PCR buffer (commercially available from Takara Shuzo), 50 mM of magnesium chloride and 100 U of a reverse transcriptase (M-MuLV RTase, commercially available from BRL) in a total volume of 10 μ l. The reaction was carried out at 37°C for 30 minutes and the reaction mixture was then heated at 95°C for 5 minutes, followed by retaining the reaction mixture in ice.

Polymerase chain reaction (PCR) was performed using the above-described cDNA as a template and 20KF and 20KR1 as primers. The reaction was performed using 10 μ l of the cDNA synthesis reaction mixture, a mixture of 50 pmol each of the primers, 200 μ M each of dATP, dCTP, dGTP and dTTP, 1 x PCR buffer (commercially available from TAKARA SHUZO), and 2.5 U of AmpliTaq DNA polymerase (commercially available from TAKARA SHUZO) in a total volume of 50 μ l. A cycle of temperature conditions of 94°C for 1 minute, 40°C for 1 minute and 72°C for 2.5 minutes was

repeated 30 times in a DNA Thermocycler (commercially available from Perkin Elmer Cetus).

The PCR product was separated on 2% agarose gel. A small number of fragments were detected by the ethidium bromide staining method. One of them had a size of 94 bp as expected.

The PCR fragment was cut out from the gel and subcloned into pUC19 plasmid. The DNA sequence of the sub-cloned PCR fragment was determined by the dideoxy method using T7 sequencing kit (commercially available from Pharmacia). Between the two primers, a DNA sequence encoding the expected amino acid sequence was observed. The nucleotide sequence of the DNA between the primers and the amino acid sequence encoded thereby are as follows.

C TCT GAC GTG AAC TGT GTT CTA TGC CCT CGC
Ser Asp Val Asn Cys Val Leu Cys Pro Arg

Isotope ^{32}P (commercially available from Amersham) was incorporated into the oligonucleotide using a DNA 5'-end labelling kit MEGALABEL (commercially available from Takara Shuzo) to obtain a radioactive oligonucleotide probe.

6. Screening of PLD Gene-containing Clones

Using the radioactive oligonucleotide as a probe, a cDNA library was screened. Hybridization solution contained 0.5 M sodium phosphate buffer (pH 7.2), 7% SDS, 1 mM EDTA and 100 $\mu\text{g/ml}$ of salmon sperm DNA, and hybridization was performed after adding the probe to the hybridization solution at 45°C for 16 hours. The washing solution contained 0.3 M NaCl and 30 mM sodium citrate, and washing was performed twice at 45°C for 20 minutes each. Positive plaques were isolated and subcloned *in vivo* into pBluescript plasmid (commercially available from Stratagene) in accordance with the instructions provided by the manufacturer of λ ZAPII cloning vector. The nucleotide sequence was determined by the dideoxy method. As a result, a region encoding the internal amino acid sequence determined in the "Section 3" existed.

7. Determination of Nucleotide Sequence of 5'-end Region

Since a clone containing the full length of cDNA could not be isolated, a DNA fragment having the 5'-end region was prepared by RACE method (Edwards et al., Nucleic Acids Res., 19, 5227-5232 (1991)). 5'-AmpliFINDER RACE Kit (commercially available from Clontech) was used in accordance with the manual attached to the product. An oligoDNA was synthesized based on the nucleotide sequence of the cDNA determined in "Section 6", and PCR was performed using the mRNA prepared by the method described in "Section 4" as a template. The PCR product was subcloned into a PCRII vector (commercially available from Invitrogen) and the nucleotide sequence was determined by the dideoxy method. The thus determined nucleotide sequence of the cDNA of rice PLD as well as the deduced amino acid sequence encoded thereby is shown in SEQ ID NO. 2 in the Sequence Listing. It is thought that translation is initiated from the 182nd nucleotide shown in SEQ ID NO. 2 since a termination codon exists at 36 bases upstream thereof.

8. Isolation of PLD Genomic Clone Corresponding to PLD cDNA and Identification of Promoter Region

To isolate a genomic DNA clone having the regulatory sequence of the PLD gene corresponding to the PLD cDNA determined in "section 6", which was cloned into pBluescript plasmid, a genomic library of rice, variety "KOSHIHIKARI" was prepared. This was carried out by partially digesting DNAs from live leaves of KOSHIHIKARI with *Mbo* I, purifying a fraction having a size of 16 - 20 kb by sucrose gradient centrifugation, and using lambda DASH II (commercially available from Stratagene) and GigapackII Gold (commercially available from Stratagene). The genomic library was screened with the PLD cDNA clone as a probe. The screening was carried out in the same manner as in "Section 6" except that hybridization was performed at 65°C for 16 hours, the washing solution contained 0.5 x SSC and 0.1% SDS, and that the washing was performed twice at 65°C for 20 minutes each. The nucleotide sequence of the hybridized genomic clone was determined by the dideoxy method. As a result, a region homologous to the cDNA sequence determined in "Section 6" existed.

The transcription initiation site was determined by the method described in "Section 7". In the vicinity of the transcription initiation site, a "TATA" consensus sequence box was observed. The ATG translation initiation site was determined based on the determined DNA sequence as the most upstream ATG codon in the translation open reading frame of the clone and as the ATG codon which is first accessible in the mRNA synthesized in rice.

The DNA sequence of a part of the genomic clone hybridized with the cDNA clone is shown in SEQ ID NO. 3. In the genomic DNA sequence, an open reading frame starting from the ATG translation initiation codon, which overlaps with the corresponding cDNA sequence has been identified. The promoter region exists upstream of the ATG translation initiation codon and starts from the site immediately upstream thereof.

9. Identification of Introns and Analysis of Functions thereof on Expression of Genes

From comparison between the cDNA (SEQ ID NO. 2) and the genomic DNA (SEQ ID NO. 3), it was proved that 3 introns exist in PLD gene. Among these, the intron having a size of 173 bp located at the 5'-flanking region of the mRNA (i.e., the nucleotide sequence between 1666nt and 1838nt of the nucleotide sequence shown in SEQ ID NO. 3, the sequence being shown in SEQ ID NO. 4) was tested for its influence on expression of a gene in plant cells. Primers of 15mer each of which contains 5 bases of exon region (5'-ACCCGGTAAGCCCAG-3', 3'-CCCCCGCGTCCATCC-5') were synthesized and PCR was carried out using the genomic clone as a template according to the method described in the Section of "5. Preparation of Probes". The PCR product was subcloned into PCRII vector and a fragment was cut out with *Eco* RI. The fragment was blunted and inserted into the *Sma* I site of a plasmid pBI221 (commercially available from Toyobo) (see Fig. 1). The obtained recombinant plasmid was introduced into rice cultured cells (Baba et al., Plant Cell Physiol. 27, 463-471 (1986)) in accordance with the reported method (Shimamoto et al., Nature, 338, 274-276 (1989)) and β -glucuronidase (GUS) activity was measured. As shown in Table 2, by introducing the intron, the GUS activity was increased. Further, as shown in Table 3, increase in the GUS activity was also observed in the case where the intron was inserted in the reverse direction. The direction of the intron was determined based on the sizes of the fragments cut out with *Bgl* II and *Bam* HI, utilizing the *Bgl* II site existing in the intron sequence and the *Bam* HI site existing in pBI221.

Table 2

Plasmid	GUS Activity
pBI221	10.4
pBI221 + intron	105.7
(pmol MU/min./mg protein)	

Table 3

Plasmid	GUS Activity
pBI221	8.8
pBI221 + intron	79.4
pBI221 + intron (reverse direction)	54.2
(pmol MU/min./mg protein)	

SEQUENCE LISTING

SEQ ID NO.: 1

SEQUENCE LENGTH: 183

SEQUENCE TYPE: Nucleic Acid

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE

ORGANISM: *Oryza sativa*

SEQUENCE DESCRIPTION

ACCCGGTAAG CCCAGTGTGC TTAGGCTAAG CGCACTAGAG CTTCTTGCTC GCTTGCTTCT 60
 TCTCCGCTCA GATCTGCTTG CTTGCTTGCT TCGCTAGAAC CCTACTCTGT GCTGCGAGTG 120
 TCGCTGCTTC GTCTTCCTTC CTCAAGTTCG ATCTGATTGT GTGTGTGGGG GGGCGCAGGT 180
 AGG 183

SEQ ID NO.: 2

SEQUENCE LENGTH: 3040

SEQUENCE TYPE: Nucleic Acid

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE

ORGANISM: *Oryza sativa*

SEQUENCE DESCRIPTION

AGTCTCTCTT CTCCCGCAAT TTTATAATCT CGATCGATCC AATCTGCTCC CCTTCTTCTT 60
 CTACTCTCCC CATCTCGGCT CTCGCCATCG CCATCCTCCT CTCCCTTCCC GGAGAAGACG 120
 CCTCCCTCCG CCGATCACCA CCCGGTAGGG CGAGGAGGGA GCCAAATCCA AATCAGCAGC 180
 C ATG GCG CAG ATG CTG CTC CAT GGG ACG CTG CAC GCC ACC ATC TTC GAG 229
 Met Ala Gln Met Leu Leu His Gly Thr Leu His Ala Thr Ile Phe Glu
 1 5 10 15
 GCG GCG TCG CTC TCC AAC CCG CAC CGC GCC AGC GGA AGC GCC CCC AAG 277
 Ala Ala Ser Leu Ser Asn Pro His Arg Ala Ser Gly Ser Ala Pro Lys

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	20	25	30	
5	TTC ATC CGC AAG TTT GTG GAG GGG ATT GAG GAC ACT GTG GGT GTC GGC			325
	Phe Ile Arg Lys Phe Val Glu Gly Ile Glu Asp Thr Val Gly Val Gly			
	35	40	45	
10	AAA GGC GCC ACC AAG GTG TAT TCT ACC ATT GAT CTG GAG AAA GCT CGT			373
	Lys Gly Ala Thr Lys Val Tyr Ser Thr Ile Asp Leu Glu Lys Ala Arg			
	50	55	60	
15	GTA GGG CGA ACT AGG ATG ATA ACC AAT GAG CCC ATC AAC CCT CGC TGG			421
	Val Gly Arg Thr Arg Met Ile Thr Asn Glu Pro Ile Asn Pro Arg Trp			
	65	70	75	80
20	TAT GAG TCG TTC CAC ATC TAT TGC GCT CAT ATG GCT TCC AAT GTG ATC			469
	Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala Ser Asn Val Ile			
	85	90	95	
25	TTC ACT GTC AAG ATT GAT AAC CCT ATT GGG GCA ACG AAT ATT GGG AGG			517
	Phe Thr Val Lys Ile Asp Asn Pro Ile Gly Ala Thr Asn Ile Gly Arg			
	100	105	110	
30	GCT TAC CTG CCT GTC CAA GAG CTT CTC AAT GGA GAG GAG ATT GAC AGA			565
	Ala Tyr Leu Pro Val Gln Glu Leu Leu Asn Gly Glu Glu Ile Asp Arg			
	115	120	125	
35	TGG CTC GAT ATC TGT GAT AAT AAC CGC GAG TCT GTT GGT GAG AGC AAG			613
	Trp Leu Asp Ile Cys Asp Asn Asn Arg Glu Ser Val Gly Glu Ser Lys			
	130	135	140	
40	ATC CAT GTG AAG CTT CAG TAC TTC GAT GTT TCC AAG GAT CGC AAT TGG			661
	Ile His Val Lys Leu Gln Tyr Phe Asp Val Ser Lys Asp Arg Asn Trp			
	145	150	155	160
45	GCG AGG GGT GTC CGC AGT ACC AAG TAT CCA GGT GTT CCT TAC ACC TTC			709
	Ala Arg Gly Val Arg Ser Thr Lys Tyr Pro Gly Val Pro Tyr Thr Phe			
50		165	170	175
55				

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	TTC TCT CAG AGG CAA GGG TGC AAA GTT ACC TTG TAC CAA GAT GCT CAT	757
5	Phe Ser Gln Arg Gln Gly Cys Lys Val Thr Leu Tyr Gln Asp Ala His	
	180 185 190	
	GTC CCA GAC AAC TTC ATT CCA AAG ATT CCG CTT GCC GAT GGC AAG AAT	805
10	Val Pro Asp Asn Phe Ile Pro Lys Ile Pro Leu Ala Asp Gly Lys Asn	
	195 200 205	
	TAT GAA CCC CAC AGA TGC TGG GAG GAT ATC TTT GAT GCT ATA AGC AAT	853
15	Tyr Glu Pro His Arg Cys Trp Glu Asp Ile Phe Asp Ala Ile Ser Asn	
	210 215 220	
	GCT CAA CAT TTG ATT TAC ATC ACT GGC TGG TCT GTA TAC ACT GAG ATC	901
20	Ala Gln His Leu Ile Tyr Ile Thr Gly Trp Ser Val Tyr Thr Glu Ile	
	225 230 235 240	
	ACC TTG GTT AGG GAC TCC AAT CGT CCA AAA CCT GGA GGG GAT GTC ACC	949
25	Thr Leu Val Arg Asp Ser Asn Arg Pro Lys Pro Gly Gly Asp Val Thr	
	245 250 255	
	CTT GGG GAG TTG CTC AAG AAG AAG GCC AGT GAA GGT GTT CGG GTC CTC	997
30	Leu Gly Glu Leu Leu Lys Lys Lys Ala Ser Glu Gly Val Arg Val Leu	
	260 265 270	
	ATG CTT GTG TGG GAT GAC AGG ACT TCA GTT GGT TTG CTA AAG AGG GAT	1045
35	Met Leu Val Trp Asp Asp Arg Thr Ser Val Gly Leu Leu Lys Arg Asp	
	275 280 285	
	GGC TTG ATG GCA ACA CAT GAT GAG GAA ACT GAA AAT TAC TTC CAT GGC	1093
40	Gly Leu Met Ala Thr His Asp Glu Glu Thr Glu Asn Tyr Phe His Gly	
	290 295 300	
	TCT GAC GTG AAC TGT GTT CTA TGC CCT CGC AAC CCT GAT GAC TCA GGC	1141
45	Ser Asp Val Asn Cys Val Leu Cys Pro Arg Asn Pro Asp Asp Ser Gly	
	305 310 315 320	
50	AGC ATT GTT CAG GAT CTG TCG ATC TCA ACT ATG TTT ACA CAC CAT CAG	1189

55

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Ser Ile Val Gln Asp Leu Ser Ile Ser Thr Met Phe Thr His His Gln
325 330 335
5 AAG ATA GTA GTT GTT GAC CAT GAG TTG CCA AAC CAG GGC TCC CAA CAA 1237
Lys Ile Val Val Val Asp His Glu Leu Pro Asn Gln Gly Ser Gln Gln
340 345 350
10 AGG AGG ATA GTC AGT TTC GTT GGT GGC CTT GAT CTC TGT GAT GGA AGG 1285
Arg Arg Ile Val Ser Phe Val Gly Gly Leu Asp Leu Cys Asp Gly Arg
15 355 360 365
TAT GAC ACT CAG TAC CAT TCT TTG TTT AGG ACA CTC GAC AGT ACC CAT 1333
Tyr Asp Thr Gln Tyr His Ser Leu Phe Arg Thr Leu Asp Ser Thr His
20 370 375 380
CAT GAT GAC TTC CAC CAG CCA AAC TTT GCC ACT GCA TCA ATC AAA AAG 1381
His Asp Asp Phe His Gln Pro Asn Phe Ala Thr Ala Ser Ile Lys Lys
25 385 390 395 400
GGT GGA CCT AGA GAG CCA TGG CAT GAT ATT CAC TCA CGG CTG GAA GGG 1429
Gly Gly Pro Arg Glu Pro Trp His Asp Ile His Ser Arg Leu Glu Gly
30 405 410 415
CCA ATC GCA TGG GAT GTT CTT TAC AAT TTC GAG CAG AGA TGG AGA AAG 1477
Pro Ile Ala Trp Asp Val Leu Tyr Asn Phe Glu Gln Arg Trp Arg Lys
35 420 425 430
CAG GGT GGT AAG GAT CTC CTT CTG CAG CTC AGG GAT CTG TCT GAC ACT 1525
Gln Gly Gly Lys Asp Leu Leu Leu Gln Leu Arg Asp Leu Ser Asp Thr
40 435 440 445
ATT ATT CCA CCT TCT CCT GTT ATG TTT CCA GAG GAC AGA GAA ACA TGG 1573
Ile Ile Pro Pro Ser Pro Val Met Phe Pro Glu Asp Arg Glu Thr Trp
45 450 455 460
50 AAT GTT CAG CTA TTT AGA TCC ATT GAT GGT GGT GCT GCT TTT GGG TTC 1621
Asn Val Gln Leu Phe Arg Ser Ile Asp Gly Gly Ala Ala Phe Gly Phe
55

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	465	470	475	480	
5	CCT GAT ACC CCT GAG GAG GCT GCA AAA GCT GGG CTT GTA AGC GGA AAG	1669			
	Pro Asp Thr Pro Glu Glu Ala Ala Lys Ala Gly Leu Val Ser Gly Lys				
	485	490	495		
10	GAT CAA ATC ATT GAC AGG AGC ATC CAG GAT GCA TAC ATA CAT GCC ATC	1717			
	Asp Gln Ile Ile Asp Arg Ser Ile Gln Asp Ala Tyr Ile His Ala Ile				
	500	505	510		
15	CGG AGG GCA AAG AAC TTC ATC TAT ATA GAG AAC CAA TAC TTC CTT GGA	1765			
	Arg Arg Ala Lys Asn Phe Ile Tyr Ile Glu Asn Gln Tyr Phe Leu Gly				
	515	520	525		
20	AGT TCC TAT GCC TGG AAA CCC GAG GGC ATC AAG CCT GAA GAC ATT GGT	1813			
	Ser Ser Tyr Ala Trp Lys Pro Glu Gly Ile Lys Pro Glu Asp Ile Gly				
	530	535	540		
25	GCC CTG CAT TTG ATT CCT AAG GAG CTT GCA CTG AAA GTT GTC AGT AAG	1861			
	Ala Leu His Leu Ile Pro Lys Glu Leu Ala Leu Lys Val Val Ser Lys				
	545	550	555	560	
30	ATT GAA GCC GGG GAA CGG TTC ACT GTT TAT GTT GTG GTG CCA ATG TGG	1909			
	Ile Glu Ala Gly Glu Arg Phe Thr Val Tyr Val Val Val Pro Met Trp				
	565	570	575		
35	CCT GAG GGT GTT CCA GAG AGT GGA TCT GTT CAG GCA ATC CTG GAC TGG	1957			
	Pro Glu Gly Val Pro Glu Ser Gly Ser Val Gln Ala Ile Leu Asp Trp				
	580	585	590		
40	CAA AGG AGA ACA ATG GAG ATG ATG TAC ACT GAC ATT ACA GAG GCT CTC	2005			
	Gln Arg Arg Thr Met Glu Met Met Tyr Thr Asp Ile Thr Glu Ala Leu				
	595	600	605		
45	CAA GCC AAG GGA ATT GAA GCG AAC CCC AAG GAC TAC CTC ACT TTC TTC	2053			
	Gln Ala Lys Gly Ile Glu Ala Asn Pro Lys Asp Tyr Leu Thr Phe Phe				
	610	615	620		
50					
55					

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	TGC TTG GGT AAC CGT GAG GTG AAG CAG GCT GGG GAA TAT CAG CCT GAA	2101
	Cys Leu Gly Asn Arg Glu Val Lys Gln Ala Gly Glu Tyr Gln Pro Glu	
5	625 630 635 640	
	GAA CAA CCA GAA GCT GAC ACT GAT TAC AGC CGA GCT CAG GAA GCT AGG	2149
10	Glu Gln Pro Glu Ala Asp Thr Asp Tyr Ser Arg Ala Gln Glu Ala Arg	
	645 650 655	
	AGG TTC ATG ATC TAT GTC CAC ACC AAA ATG ATG ATA GTT GAC GAT GAG	2197
15	Arg Phe Met Ile Tyr Val His Thr Lys Met Met Ile Val Asp Asp Glu	
	660 665 670	
	TAC ATC ATC ATC GGT TCT GCA AAC ATC AAC CAG AGG TCG ATG GAC GGC	2245
20	Tyr Ile Ile Ile Gly Ser Ala Asn Ile Asn Gln Arg Ser Met Asp Gly	
	675 680 685	
	GCT AGG GAC TCT GAG ATC GCC ATG GGC GGG TAC CAG CCA TAC CAT CTG	2293
25	Ala Arg Asp Ser Glu Ile Ala Met Gly Gly Tyr Gln Pro Tyr His Leu	
	690 695 700	
	GCG ACC AGG CAA CCA GCC CGT GGC CAG ATC CAT GGC TTC CGG ATG GCG	2341
30	Ala Thr Arg Gln Pro Ala Arg Gly Gln Ile His Gly Phe Arg Met Ala	
	705 710 715 720	
	CTG TGG TAC GAG CAC CTG GGA ATG CTG GAT GAT GTG TTC CAG CGC CCC	2389
35	Leu Trp Tyr Glu His Leu Gly Met Leu Asp Asp Val Phe Gln Arg Pro	
	725 730 735	
	GAG AGC CTG GAG TGT GTG CAG AAG GTG AAC AGG ATC GCG GAG AAG TAC	2437
40	Glu Ser Leu Glu Cys Val Gln Lys Val Asn Arg Ile Ala Glu Lys Tyr	
	740 745 750	
	TGG GAC ATG TAC TCC AGC GAC GAC CTC CAG CAG GAC CTC CCT GGC CAC	2485
45	Trp Asp Met Tyr Ser Ser Asp Asp Leu Gln Gln Asp Leu Pro Gly His	
	755 760 765	
50	CTC CTC AGC TAC CCC ATT GGC GTC GCC AGC GAT GGT GTG GTG ACT GAG	2533
55		

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Leu Leu Ser Tyr Pro Ile Gly Val Ala Ser Asp Gly Val Val Thr Glu

770

775

780

CTG CCC GGG ATG GAG TAC TTT CCT GAC ACA CGG GCC CGC GTC CTC GGC 2581

Leu Pro Gly Met Glu Tyr Phe Pro Asp Thr Arg Ala Arg Val Leu Gly

785

790

795

800

GCC AAG TCG GAT TAC ATG CCC CCC ATC CTC ACC TCA TAGACGAGGA AGCACT 2633

Ala Lys Ser Asp Tyr Met Pro Pro Ile Leu Thr Ser

805

810

ACACTACAAT CTGCTGGCTT CTCCTGTCAG TCCTTCTGTA CTTCTTCAGT TTGGTGGCGA 2693

GATGGTATGG CCGTTGTTCA GAATTTCTTC AGAATAGCAG TTGTTACAGT TGTGAATCAT 2753

AAAGTAATAA GTGCAGTATC TGTGCATGGT TGAGTTGGGA AGAAGATCGG GGATGCAATG 2813

ATGCTTGTGA AGTTGTGATG CCGTTTGTA GATGGGAAGT TGGGAACTAC TAAGTAATTG 2873

GCATGATTGT ACTTTGCACT ACTGTTTAGC GTTGTGATA CTGGTTAACC GTGTGTTTCA 2933

CTGAACCTGA TTCTTGATGC AGTTTGTGGC ATTACCAGTT TATCATCGTT CTTCAGGAAA 2993

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 3040

SEQ ID NO.: 3

SEQUENCE LENGTH: 2799

SEQUENCE TYPE: Nucleic Acid

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE

ORGANISM: *Oryza sativa*

SEQUENCE DESCRIPTION

CAAGGGTGTA CATAGATTTG TCTCGTAAAA TAGTATTATA ATATTATAAA CTTATTACTC 60

TATCCGTTCT AAAATATAAG AACCTTATGA CTGGATGGAA CATTTCCTAG TACTACGAAT 120

CTGAACACAT GTCTAGATTC ATAGTACTAG GAAATGTCTC ATCGCGGTAC TAGGTTCTTA 180

TATTTTAGGA TGGAGGGAGT TTAATATAAA ACTAATGGTT AGAACTTTGA AAGTTTGATT 240

TTAAATGTCA AATATTTATG GCTGGAGGTA GTATAATATG TTTTTTTTGG GACGTAGACT 300

AGGTAGTATA ATATGTTTGG TTGTGTTTAG ATCCAATATT TGGATCCAAA CTTCACTCAT 360

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TTTCCATCAC ATCAACTTGT CATATACACA TAACTTTTCA GTCACATCAT CCCCAATTTT 420
 AACCAAAATC AAACCTTTGCG CTGAACTAAA CACAACCTTT GGGCCCGTTT AGTTCCCCAA 480
 TTTTTTTCCC AAAAACATCA CATCGAATCT TTGGACACAT GCATGAAGCA TTAAATATAG 540
 ATAAAAAGAA AAACCTAATTG CACAGTTATG GAGGAAATCG CGAGACGAAT CTTTAAAGCC 600
 TAATTAGTCC GTGATTAGCC ATAAGTGCTA CAGTAACCCA ATTGTGCTAA TGACGGCTTA 660
 ATTAGTCTCC ACAAGATTGG TCTCGCAGTT TCCAGGCGAG TTCTGAAATT AGTTTTTTTCA 720
 TTCGTGTCCG AAAACCCCTT CCGACATCCG GTCAAACGTT CGATATGACA CCCACAAATT 780
 TTCTTTTCCC CAACTAAACA CACCCTTTAT CTCTTACCCT CTGGCTCTTT CAGTAGGCAT 840
 ATCCAAGACA GCTGGTAATG CAGGCTCGGA CATAATTTGA CAGTTACGTT CATGTGACCG 900
 ACGGTTGATG CTAGTGCAAC TGCAACATAC TGTTGAGATG GATGTCCCAA CGAGCTCAAA 960
 ACAACTTAGG TGGCGCGTCG CGATTTCATCA ATAACCTAAA TGGAAGCGCA AGTGACGTA 1020
 CGAAAATGAC AGCGAGTGAG GTGGCGAGCC TCACCTTGGT GATCCCAACC GGATAAGCTA 1080
 TGCATCAGCC AGTTTTCGTGG GGCTGCACAT TTCGTGCAAC ACCTGGAGTC CACGCCGCCG 1140
 GCGACGTCGG CACAGCGCGC CCGCCCACCG CCCACGCACG CGCTTGACTC CACCCATGTT 1200
 CTCCCTTCTC GACGCCCGCG AAGCCAGCGA ACCGATCCGA GGAAGTCAAG CCCCCACCGC 1260
 CACTTGGACC GACCTCGGGA CGACGACGCC CCCGCGCTCT TCTAGACGCG CGGACGACGC 1320
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 CTACCCGTTT TTAACCTCGC CTCCTCCTCC TCCCGGCTCG AGATCCGTGG CCACGACGCG 1440
 TGGTGGGAAA CCGGGAACGA CGTGCACGCA CGCACACAGG GCAAGTTTCA GTAGAAAAAT 1500
 CGCCGGCATC CAGATCGGGA CAGTCTCTCT TCTCCCGCAA TTTTATAATC TCGCTCGATC 1560
 CAATCTGCTC CCCTTCTTCT TCTACTCTCC CCATCTCGGC TCTCGCCATC GCCATCCTCC 1620
 TCTCCCTTCC CGGAGAAGAC GCCTCCCTCC GCCGATCACC ACCCGGTAAG CCCAGTGTGC 1680
 TTAGGCTAAG CGCACTAGAG CTTCTTGCTC GCTTGCTTCT TCTCCGCTCA GATCTGCTTG 1740
 CTTGCTTGCT TCGCTAGAAC CCTACTCTGT GCTGCGAGTG TCGCTGCTTC GTCTTCCTTC 1800
 CTCAAGTTGG ATCTGATTGT GTGTGTGGGG GGGCGCAGGT AGGGCGAGGA GGGAGCCAAA 1860
 TCCAAATCAG CAGCC ATG GCG CAG ATG CTG CTC CAT GGG ACG CTG CAC GCC 1911

Met Ala Gln Met Leu Leu His Gly Thr Leu His Ala

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ACC ATC TTC GAG GCG GCG TCG CTC TCC AAC CCG CAC CGC GCC AGC GGA 1959
 Thr Ile Phe Glu Ala Ala Ser Leu Ser Asn Pro His Arg Ala Ser Gly
 5 15 20 25

AGC GCC CCC AAG TTC ATC CGC AAG GTTCGGACCC TTCTCCTTAA TCTACTCGTC 2013
 Ser Ala Pro Lys Phe Ile Arg Lys
 10 30 35

TTTGCTCTTG CTCTTTTCT TTTGTGTCCC TTTCTTGTGT GTGCGTTTGC ATGAGCCCGA 2073
 15 ATTTGATCTG CTAGTGCACA GTACAGTCAG ATACACTGAA ACGATCTGGA AATTCTGGAT 2133
 TATTAGGAAA AATAAAGAGG TAGTAGACAA GAATTGGAGA TACTTTCTAT CAAGATTGGT 2193
 CTATTATGCT TGGCCATTTC TTGTTTGACC CAAGTACTTC TTTGAATCTA GAGTTTGCTG 2253
 20 TGTGTGATGT GGTGTGTGTT TGTGTCACCA AAAATCTTCA TTAGCTAAAA CTGAAATTTT 2313
 ATTTATTAAC TGACCTACTA AAAATGTAGA GTTCTCTGTG TGTGATGTGT GCTTGTGTCA 2373
 CCAAAAATCT TGATTGATA GAGTTTTTAT TTATTTATTA ACTGACCTAC TACAAATCTA 2433
 25 TTGCTGTATG CTATGTGTGT CTGTATCACC TGAAATGCAA TGTCTTCTTC TTTGTTGTTT 2493
 TTGATCTAAC ACGTGAGCTC ATGTCAACAG TTT GTG GAG GGG ATT GAG GAC ACT 2547
 Phe Val Glu Gly Ile Glu Asp Thr
 30 40

GTG GGT GTC GGC AAA GGC GCC ACC AAG GTG TAT TCT ACC ATT GAT CTG 2595
 35 Val Gly Val Gly Lys Gly Ala Thr Lys Val Tyr Ser Thr Ile Asp Leu
 45 50 55 60

GAG AAA GCT CGT GTA GGG CGA ACT AGG ATG ATA ACC AAT GAG CCC ATC 2643
 40 Glu Lys Ala Arg Val Gly Arg Thr Arg Met Ile Thr Asn Glu Pro Ile
 65 70 75

AAC CCT CGC TGG TAT GAG TCG TTC CAC ATC TAT TGC GCT CAT ATG GCT 2691
 45 Asn Pro Arg Trp Tyr Glu Ser Phe His Ile Tyr Cys Ala His Met Ala
 80 85 90

TCC AAT GTG ATC TTC ACT GTC AAG ATT GAT AAC CCT ATT GGG GCA ACG 2739
 50 Ser Asn Val Ile Phe Thr Val Lys Ile Asp Asn Pro Ile Gly Ala Thr
 55

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95 100 105

AAT ATT GGG AGG GCT TAC CTG CCT GTC CAA GAG CTT CTC AAT GGA GAG 2787

Asn Ile Gly Arg Ala Tyr Leu Pro Val Gln Glu Leu Leu Asn Gly Glu

110	115	120	
GAG ATT GAC AGA			2799
Glu Ile Asp Arg			

125

SEO ID NO.: 4

SEQUENCE LENGTH: 173

SEQUENCE TYPE: Nucleic Acid

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE

ORGANISM: *Oryza sativa*

SEQUENCE DESCRIPTION

GTAAGCCCAG TGTGCTTAGG CTAAGCGCAC TAGAGTTCT TGCTCGCTTG CTTCTTCTCC 60
 GCTCAGATCT GCTTGCTTGC TTGCTTCGCT AGAACCCTAC TCTGTGCTGC GAGTGTCGCT 120
 GCITCGTCTT CCTTCCTCAA GTTCGATCTG ATTGTGTGTG TGGGGGGGCG CAG 173

Claims

1. An isolated DNA fragment having a nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing or having a nucleotide sequence which is the same as the nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing except that one or a plurality of nucleotides are added, inserted, deleted or substituted, the latter nucleotide sequence having a function to promote expression of a gene downstream thereof.
2. The DNA fragment according to claim 1, which has a nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing.
3. An isolated DNA fragment having a nucleotide sequence shown in SEQ ID NO. 4 in Sequence Listing or having a nucleotide sequence which is the same as the nucleotide sequence shown in SEQ ID NO. 4 in Sequence Listing except that one or a plurality of nucleotides are added, inserted, deleted or substituted, the latter nucleotide sequence having a function to promote expression of a gene downstream thereof.
4. The DNA fragment according to claim 3, which has a nucleotide sequence shown in SEQ ID NO. 4 in Sequence Listing.
5. A recombinant vector comprising said DNA fragment according to claim 1 and a foreign gene to be expressed, which is operably linked to said DNA fragment at a downstream region of said DNA fragment.

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6. The recombinant vector according to claim 5, wherein said DNA fragment has a nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing.
- 5 7. The recombinant vector according to claim 6, wherein said DNA fragment has a nucleotide sequence shown in SEQ ID NO. 4 in Sequence Listing.
8. A method for expressing a foreign gene comprising introducing said recombinant vector according to claim 3 into host cells and expressing said foreign gene.
- 10 9. The method according to claim 8, wherein said DNA fragment has a nucleotide sequence shown in SEQ ID NO. 1 in Sequence Listing.
10. The method according to claim 8, wherein said DNA fragment has a nucleotide sequence shown in SEQ ID NO. 4 in Sequence Listing.

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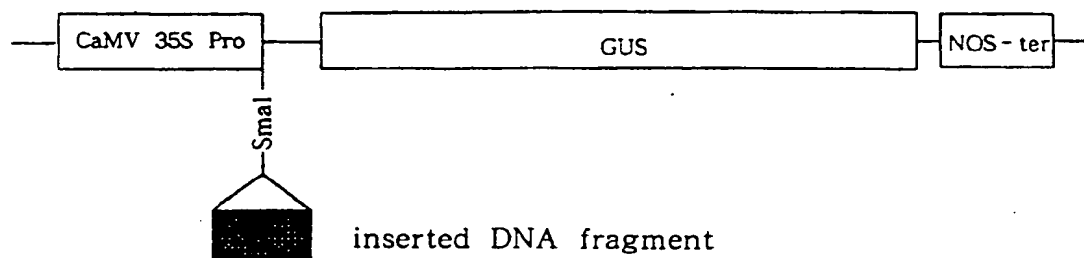


Fig. 1

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP96/00812

A. CLASSIFICATION OF SUBJECT MATTER Int. Cl ⁶ C12N15/11, C12N15/63, C12N15/82, C12N9/16 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int. Cl ⁶ C12N15/00, C12N9/16 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) CAS ONLINE, WPI, WPI/L, BIOSIS PREVIEWS		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	JP, 03-103182, A (Mitsubishi Kasei Corp.), April 30, 1991 (30. 04. 91) (Family: none)	1 - 10
A	Judy C. et al. "Introns increase gene expression in cultured maize cells" GENE & DEVELOPMENT (1987) Vol. 1, p. 1183-1200	1 - 10
A	Akira T. et al. "Enhancement of foreign gene expression by a dicot intron in rice but not in tobacco in correlated with an increased level of mRNA and an efficient splicing of the intron" Nucleic Acids Research (1990) Vol. 18, No. 23, p. 6767-6770	1 - 10
PA	Jun U. et al. "Purification and Characterization of Phospholipase D (PLD) from rice (Oryza sativa L.) and Cloning of cDNA for PLD from Rice and Maize (Zeamays L.)" Plant Cell Physiol. (1995) Vol. 36, No. 5, p. 903-914	1 - 10
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search June 19, 1996 (19. 06. 96)		Date of mailing of the international search report July 2, 1996 (02. 07. 96)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.

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